

SEQUENCE LISTING

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Nicola, Nicos A.
Hilton, Douglas J.
Metcalf, Donald
Zhang, Jian G.

<120> NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
ENCODING SAME

<130> Davies cc

<140> 09/051,843
<141> 1998-06-29

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<170> PatentIn Ver. 2.0

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 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
 20 25 30

cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata 204
 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
 35 40 45

tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga 252
Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
50 55 60

tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa 300
 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
 65 70 75 80

act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag 348
 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
 85 90 95

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gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg      396
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 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
 115 120 125

act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc 492
 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser

tgg	ctc	cct	gga	agg	aat	aca	agc	cct	gac	aca	cac	tat	act	ctg	tac	540
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Tyr	Trp	Tyr	Ser	Ser	Leu	Glu	Lys	Ser	Arg	Gln	Cys	Glu	Asn	Ile	Tyr	
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Val	Lys	Pro	Asp	Pro	Pro	His	Ile	Lys	His	Leu	Leu	Leu	Lys	Asn	Gly	
					225			230			235			240		
gcc	tta	tta	gtg	cag	tgg	aag	aat	cca	caa	aat	ttt	aga	agc	aga	tgc	828
Ala	Leu	Leu	Val	Gln	Trp	Lys	Asn	Pro	Gln	Asn	Phe	Arg	Ser	Arg	Cys	
					245				250			255				
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Leu	Thr	Tyr	Glu	Val	Glu	Val	Asn	Asn	Thr	Gln	Thr	Asp	Arg	His	Asn	
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Ile	Leu	Glu	Val	Glu	Glu	Asp	Lys	Cys	Gln	Asn	Ser	Glu	Ser	Asp	Arg	
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Asn	Met	Glu	Gly	Thr	Ser	Cys	Phe	Gln	Leu	Pro	Gly	Val	Leu	Ala	Asp	
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gct	gtc	tac	aca	gtc	aga	gtg	aaa	aca	aac	aag	tta	tgc	ttt		1020	
Ala	Val	Tyr	Thr	Val	Arg	Val	Arg	Val	Lys	Thr	Asn	Lys	Leu	Cys	Phe	
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gat	gac	aac	aaa	ctg	tgg	agt	gat	tgg	agt	gaa	gca	cag	agt	ata	ggt	1068
Asp	Asp	Asn	Lys	Leu	Trp	Ser	Asp	Trp	Ser	Glu	Ala	Gln	Ser	Ile	Gly	
					325				330			335				
aag	gag	caa	aac	tcc	acc	ttc	tac	acc	acc	atg	tta	ctc	acc	att	cca	1116
Lys	Glu	Gln	Asn	Ser	Thr	Phe	Tyr	Thr	Thr	Met	Leu	Leu	Thr	Ile	Pro	

gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg		1164	
Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg			
355	360	365	
ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt		1212	
Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe			
370	375	380	
aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag		1260	
Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys			
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tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg		1308	
Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val			
405	410	415	
ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc		1358	
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35 40 45

Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg

Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
65 70 75 80

Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
85 90 95

Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
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Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
115 120 125

Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
130 135 140

Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
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Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
165 170 175

Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
180 185 190

Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
195 200 205

Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
210 215 220

Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
225 230 235 240

Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
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Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
260 265 270

Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
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Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
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Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
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Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
340 345 350

Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
355 360 365

Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
370 375 380

Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
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<222> (61)..(1338)

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1 5 10 15

gcc ggc ggc ggg ggc ggg ggc ggc gcg cct acg gaa act cag cca 156
Ala Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
20 25 30

cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata 204
Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
35 40 45

tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg 252
Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
50 55 60

tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa 300
Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu

act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa	348		
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85	90	95	
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Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu			
100	105	110	
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115	120	125	
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Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr			
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tat tgg cac aga agc ctg gaa aaa att cat caa tgt gaa aac atc ttt	588		
Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe			
165	170	175	
aga gaa ggc caa tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag	636		
Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys			
180	185	190	
cag tcc agt ttt gaa caa cac agt gtc caa ata atg gtc aag gat aat	684		
Gln Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn			
195	200	205	
gca gga aaa att aaa cca tcc ttc aat ata gtg cct tta act tcc cgt	732		
Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg			
210	215	220	
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Val Lys Pro Asp Pro His Ile Lys Asn Leu Ser Phe His Asn Asp			
225	230	235	240
gac cta tat gtg caa tgg gag aat cca cag aat ttt att agc aga tgc	828		
Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys			
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cta ttt tat gaa gta gaa gtc aat aac agc caa act gag aca cat aat	876		
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260	265	270	
gtt ttc tac gtc caa gag gct aaa tgt gag aat cca gaa ttt gag aga	924		
Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg			

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Thr	Leu	Asn	Thr	Val	Arg	Ile	Arg	Val	Lys	Thr	Asn	Lys	Leu	Cys	Tyr	
305						310				315				320		
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Glu	Asp	Asp	Lys	Leu	Trp	Ser	Asn	Trp	Ser	Gln	Glu	Met	Thr	Ile	Val	
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Lys	Lys	Arg	Asn	Ser	Thr	Leu	Tyr	Ile	Thr	Met	Leu	Leu	Ile	Val	Pro	
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gtc	atc	gtc	gca	ggt	gca	atc	ata	gta	ctc	ctg	ctt	tac	cta	aaa	agg	1164
Val	Ile	Val	Ala	Gly	Ala	Ile	Ile	Val	Leu	Leu	Leu	Tyr	Leu	Lys	Arg	
						355			360				365			
ctc	aag	att	att	ata	ttc	cct	cca	att	cct	gat	cct	ggc	aag	att	ttt	1212
Leu	Lys	Ile	Ile	Ile	Phe	Pro	Pro	Ile	Pro	Asp	Pro	Gly	Lys	Ile	Phe	
						370			375				380			
aaa	gaa	atg	ttt	gga	gac	cag	aat	gat	gat	act	ctg	cac	tgg	aag	aag	1260
Lys	Glu	Met	Phe	Gly	Asp	Gln	Asn	Asp	Asp	Thr	Leu	His	Trp	Lys	Lys	
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tac	gac	atc	tat	gag	aag	caa	acc	aag	gag	gaa	acc	gac	tct	gta	gtg	1308
Tyr	Asp	Ile	Tyr	Glu	Lys	Gln	Thr	Lys	Glu	Glu	Thr	Asp	Ser	Val	Val	
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ctg	ata	gaa	aac	ctg	aag	aaa	gcc	tct	cag	tgatggagat	aatttatttt					1358
Leu	Ile	Glu	Asn	Leu	Lys	Lys	Ala	Ser	Gln							
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Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
35 40 45

Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
50 55 60

Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
65 70 75 80

Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
85 90 95

Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
100 105 110

Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
115 120 125

Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
130 135 140

Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
145 150 155 160

Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe
165 170 175

Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys
180 185 190

Gln Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn
195 200 205

Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg
210 215 220

Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp
225 230 235 240

Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys
245 250 255

Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn
260 265 270

Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg
275 280 285

Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp
290 295 300

Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr
305 310 315 320

Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Thr Ile Val
325 330 335

Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro
340 345 350

Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg
355 360 365

Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
370 375 380

Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
385 390 395 400

Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val
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Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
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